

Sequence Listing

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 30 bulgaricus; ZF0050544= Phyllobacterium rubiacearum; ZF0002852=
 Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862=
 Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0002031=
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
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 ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018=
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 35 40 45

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15 Gly His Val Gly Ile Gln Leu Leu Arg His Leu Ser Pro Ala Arg Ile
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 115 120 125

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	Streptomyces diatsatochromogenes; ZF0003768= Actinomyces;		
	ZF0002379= Streptomyces coelestis; ZF0002443= Streptomyces;		
	ZF0002442= Streptomyces; ZF0002436= Streptomyces; ZF0050994=		
	Bacterium; ZF0050992= Bacterium; ZF0050442= Bacterium;		
25	ZF0002049= Streptomyces; ZF0006069= Streptomyces; ZF0006075=		
	Streptomyces; ZF0004724= Nocardiaform; ZF0002392= Actinoplanes		
	nipponensis; ZF0002356= Actinoplanes brasiliensis; ZF0003501=		
	Actinomyces; ZF0051322= Bacterium; ZF0006078= Streptomyces;		
	ZF0006092= Streptomyces; ZF0006090= Streptomyces; ZF0006084=		
30	Streptomyces; ZF0006068= Streptomyces; ZF0050284= Rhodococcus;		
	ZF0050028= Agrobacterium tumefaciens; ZF0003540= Actinomyces;		
	ZF0003528= Actinomyces; ZF0003529= Actinomyces;		
	<400> 16		
35	Gly Leu Thr Ile Gly His Glu Pro Val Gly Val Ile Glu Lys Leu Gly 1 5 10 15		
40	Ser Ala Val Thr Gly Tyr Arg Glu Gly Gln Arg Val Ile Ala Gly Ala 20 25 30		
45	Ile Cys Pro Asn Phe Asn Ser Tyr Ala Ala Gln Asp Gly Ala Pro Ser 35 40 45		
50	Gln Asp Gly Ser Tyr Leu Val Ala Ser Gly Ala Cys Gly Cys His Gly 50 55 60		
55	Tyr Arg Ala Thr Ala Gly Trp Arg Phe Gly Asn Ile Ile Asp Gly Ala 65 70 75 80		
	Gln Ala Glu Tyr Leu Leu Val Pro Asp Ala Gln Gly Asn Leu Ala Pro 85 90 95		

Val Pro Asp Asn Leu Ser Asp Glu Gln Val Leu Met Cys Pro Asp Ile
100 105 110

5
Met Ser Thr Gly Phe Lys Gly Ala Glu Asn Ala His Ile Arg Ile Gly
115 120 125

10 Asp Thr Val Ala Val Phe Ala Gln Gly Pro
130 135

<210> 17

15 <211> 144

<212> PRT

20 <213> unknown

<220>

<221> source

25 <223> ZF0050197= Pseudomonas oleovorans; ZF0050294= Rhodococcus;
ZF0050330= Bacillus, ZF0002852= Rhodococcus; ZF0050310=
Arthrobacter paraffineus; ZF0002437= Streptomyces; ZF0003712=
Micromonospora; ZF0003765= Streptomyces; ZF0002332=
Streptomyces diastatochromogenes; ZF0003768= Actinomyces;
30 ZF0002379= Streptomyces coelestis; ZF0002443= Streptomyces;
ZF0002442= Streptomyces; ZF0002436= Streptomyces; ZF0050994=
Bacterium; ZF0050992= Bacterium; ZF0050442= Bacterium;
ZF0002049= Streptomyces; ZF0006069= Streptomyces; ZF0006075=
Streptomyces; ZF0004724= Nocardiaform; ZF0002392= Actinoplanes
35 nipponensis; ZF0002356= Actinoplanes brasiliensis; ZF0003501=
Actinomyces; ZF0051322= Bacterium; ZF0006078= Streptomyces;
ZF0006092= Streptomyces; ZF0006090= Streptomyces; ZF0006084=
Streptomyces; ZF0006068= Streptomyces; ZF0050284= Rhodococcus;
ZF0050028= Agrobacterium tumefaciens; ZF0003540= Actinomyces;
40 ZF0003528= Actinomyces; ZF0003529= Actinomyces;

<400> 17

Cys Gly Thr Asp Leu His Ile Leu Gly Gly Asp Val Pro Glu Val Thr
45 1 5 10 15

Asp Gly Arg Ile Leu Gly His Glu Ala Val Gly Thr Val Val Glu Val
20 25 30

50 Gly Asp Gly Val Gln Thr Leu Ala Pro Gly Asp Arg Val Leu Val Ser
35 40 45

55 Cys Val Thr Ala Cys Gly Thr Cys Arg Phe Cys Arg Glu Ser Arg Tyr
50 55 60

Gly Gln Cys Leu Gly Gly Gly Gly Trp Ile Leu Gly His Leu Ile Asp
 65 70 75 80

5 Gly Thr Gln Ala Glu Leu Val Arg Val Pro Tyr Ala Asp Asn Ser Thr
 85 90 95

10 His Arg Ile Pro Asp Gly Val Ser Asp Glu Gln Met Leu Met Leu Ala
 100 105 110

15 Asp Ile Leu Pro Thr Ser Tyr Glu Val Gly Val Leu Asn Gly Cys Leu
 115 120 125

20 Arg Pro Ala Asp Val Val Val Ile Ile Gly Ala Asp Asp Arg Pro Leu
 130 135 140

<210> 18

<211> 73

25 <212> PRT

<213> unknown

30 <220>

<221> source

<223> ZF0050310= *Arthrobacter paraffineus*

35 <400> 18

Val Asp Val Val Val Asp Asn Ala Gly Phe Gly Thr His Gly Ala Phe
 1 5 10 15

40 Val Asp Glu Asp His Glu Arg Val Thr Ser Glu Ile Gln Leu Asn Ile
 20 25 30

45 Ala Thr Leu Val Glu Leu Thr His Thr Phe Pro Pro Asp Leu Leu Thr
 35 40 45

Gly Arg Gly Ala Leu Val Asn Ile Ala Ser Thr Ala Ser Phe Gln Pro
 50 55 60

5 Thr Pro Gly Met Ala Val Tyr Cys Ala
 65 70

<210> 19
 10 <211> 75
 <212> PRT

15 <213> unknown
 <220>

<221> source
 20 <223> ZF0050310= *Arthrobacter paraffineus*
 <400> 19

Val Asp Val Val Val His Asn Ala Gly Phe Gly Thr His Gly Ala Phe
 25 1 5 10 15

Val Asp Glu Asp Leu Glu Arg Val Thr Ser Glu Ile Gln Leu Asn Ile
 30 20 25 30

Ala Thr Leu Val Glu Leu Thr His Thr Phe Leu Pro Asp Leu Leu Thr
 35 35 40 45

35 Gly Arg Gly Ala Leu Val Asn Ile Ala Ser Thr Ala Ser Phe Gln Pro
 50 55 60

40 Thr Pro Gly Met Ala Val Tyr Cys Ala Thr Lys
 65 70 75

<210> 20
 45 <211> 79
 <212> PRT

50 <213> unknown
 <220>

<221> source
 55 <223> ZF0003535= *Actinomyces*
 <400> 20

Arg Val Asp Val Val Val His Asn Ala Ala Ile Thr Gln Lys Ala Thr

19

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5	Phe Arg Asp	Ile Thr Pro Ala Asp	Phe Glu Arg Ile Leu Arg Val Asn			
		20	25	30		
10	Leu Thr Gly	Val Phe Asn Leu Ser Gln Ala Val Ile	Pro Leu Met Ile			
		35	40	45		
15	Gln Arg Gly Gly Gly Ser	Ile Val Ser Ile Ser Ser	Leu Ser Ala Gln			
		50	55	60		
20	Asn Gly Gly Gly Ile	Phe Gly Gly Ala His Tyr Cys Ala Thr Lys				
		65	70	75		
25	<210>	21				
	<211>	76				
30	<212>	PRT				
	<213>	unknown				
35	<220>					
	<221>	source				
	<223>	ZF0003535= Actinomyces				
	<400>	21				
40	Val Asp Val Val Val Asp Asn Ala Gly	Leu Ala Leu Gly Thr Ala Pro				
		1	5	10	15	
45	Ala Pro Gln Val Pro Leu Lys Asp Trp Gln Thr Met Val Asn Thr Asn					
		20	25	30		
50	Ile Thr Gly	Leu Leu Asn Ile Thr His His Leu Leu Pro Thr Leu Ile				
		35	40	45		
55	Asp Arg Lys Gly Ile Val Val Asn Leu Ser Ser Val Ala Ala His Tyr					
		50	55	60		
	Pro Tyr Thr Gly Gly Asn Val Tyr Cys Ala Ser Lys					
		65	70	75		
	<210>	22				
	<211>	72				

<212> PRT
 <213> unknown
 5 <220>
 <221> source
 <223> ZF0050310= Arthrobacter paraffineus
 10 <400> 22
 Gln Gly Ile Gly Tyr Ala Thr Ala Lys Arg Leu Ile Ser Leu Gly Ala
 1 5 10 15
 15
 Thr Val Ala Ile Gly Asp Ile Asp Glu Ala Thr Leu Ala Arg Ala Ala
 20 25 30
 20
 Lys Asp Leu Gly Ile Arg Thr Phe Gly Arg Leu Asp Val Thr Asp Pro
 35 40 45
 25
 Ala Ser Phe Phe Asp Phe Leu Asp Thr Val Glu Gly Glu Leu Gly Pro
 50 55 60
 30
 Ile Asp Val Leu Ile Asn Asn Ala
 65 70
 <210> 23
 35 <211> 75
 <212> PRT
 <213> unknown
 40 <220>
 <221> source
 <223> ZF0050310= Arthrobacter paraffineus
 45 <400> 23
 Gln Arg Ile Gly Leu Glu Ile Ala Arg Thr Phe Ile Lys Glu Gly Ala
 1 5 10 15
 50
 Thr Val Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val
 20 25 30
 55
 Ala Glu Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val
 35 40 45

Arg Asp Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala
 50 55 60

5 Phe Gly Pro Val Asp Val Met Met Asn Asn Ala
 65 70 75

10 <210> 24
 <211> 72
 <212> PRT

15 <213> unknown
 <220>

20 <221> source
 <223> ZF0050310= *Arthrobacter paraffineus*
 <400> 24

25 Gln Gly Ile Gly Tyr Gln Thr Ala Lys Glu Leu Ile Arg Arg Gly His
 1 5 10 15

30 Arg Val Ala Ile Gly Asp Ile Asp Glu Ala Arg Ala Lys Glu Thr Ala
 20 25 30

35 Ala Glu Leu Gly Val Lys Val Val Thr Arg Leu Asp Val Thr Asp Pro
 35 40 45

40 Asp Ser Phe Lys Asp Phe Leu Asp Leu Val Glu Gly Asp Leu Gly Pro
 50 55 60

45 Leu Asp Val Leu Ile Asn Asn Ala
 65 70

50 <210> 25
 <211> 74
 <212> PRT

55 <213> unknown
 <220>

<221> source
 <223> ZF0050310= *Arthrobacter paraffineus*
 <400> 25

Gly Ile Gly Leu Glu Ile Ala Arg Thr Phe Ile Lys Glu Gly Ala Thr
 1 5 10 15
 5 Val Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val Ala
 20 25 30
 10 Glu Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val Arg
 35 40 45
 15 Asp Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala Phe
 50 55 60
 20 Gly Pro Val Asp Val Ile Val Asn Asn Ala
 65 70
 <210> 26
 <211> 74
 25 <212> PRT
 <213> unknown
 30 <220>
 <221> source
 <223> ZF0050310= *Arthrobacter paraffineus*
 35 <400> 26
 Ile Gly Leu Glu Ile Ala Arg Thr Phe Ile Lys Glu Gly Ala Thr Val
 1 5 10 15
 40 Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val Gly Glu
 20 25 30
 45 Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val Arg Asp
 35 40 45
 50 Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala Phe Gly
 50 55 60
 55 Pro Val Asp Val Met Val Asn Asn Ala Gly
 65 70
 <210> 27
 <211> 62

<212> PRT
 <213> unknown
 5 <220>
 <221> source
 <223> ZF0002333= Rhodococcus erythropolis
 10 <400> 27
 Val Pro Val Ala Val Val Asp Leu His Ile Glu Ser Ala Lys Glu Thr
 1 5 10 15
 15
 Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala Leu Ala Leu Glu
 20 20 25 30
 Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala Phe Glu Ala Thr
 35 40 45
 25
 Val Ala Glu Trp Gly Arg Phe Asp Tyr Leu Val Asn Asn Ala
 50 55 60
 30 <210> 28
 <211> 74
 <212> PRT
 35 <213> unknown
 <220>
 40 <221> source
 <223> ZF0002333= Rhodococcus erythropolis
 <400> 28
 45 Leu Gly Arg Glu Ile Ala Leu Lys Leu Ala Ser Glu Gly Ala Ser Val
 1 5 10 15
 Val Val Asn Asp Leu Asp Pro Glu Pro Ala Ala Gln Thr Glu Arg Asp
 50 20 25 30
 Ile Lys Ala Thr Gly Gly Gln Ala Val Ser Cys Val Gly Ser Val Ala
 55 35 40 45
 Glu Asp Gly Phe Ala Glu Arg Phe Val Asn Thr Ala Val Glu Ser Phe
 50 55 60

Gly Gly Leu Asp Val Met Val Asn Asn Ala
 65 70

5
 <210> 29
 <211> 76

10
 <212> PRT
 <213> unknown
 <220>

15
 <221> source
 <223> ZF0002333= Rhodococcus erythropolis
 <400> 29

20
 Ala Gly Leu Gly Val Glu Phe Ala His Arg Phe Ala Ala Arg Gly Ala
 1 5 10 15

25
 Asn Leu Val Leu Val Ala Arg Arg Ala Asp Arg Leu Glu Ala Leu Ala
 20 25 30

30
 Thr Glu Leu Arg Val Ala His Gly Ile Thr Val Thr Val Leu Pro Ala
 35 40 45

35
 Asp Leu Ala Ala Pro Gly Val Gly Ala Thr Leu His Gln Glu Leu Thr
 50 55 60

40
 Ser Arg Gly Ile Thr Val Thr Ser Leu Ile Asn Asn
 65 70 75

45
 <210> 30
 <211> 72
 <212> PRT
 <213> unknown
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50
 <221> source
 <223> ZF0003535= Actinomyces
 <400> 30

55
 Pro Ala Asp Gly Tyr Gln Thr Ala Lys Glu Leu Ile Arg Arg Gly His
 1 5 10 15

25

Arg Val Ala Ile Val Asp Ile Asp Glu Ala Arg Ala Lys Gly Ala Ala
 20 25 30

5 Ala Glu Leu Gly Val Lys Val Val Thr Arg Leu Asp Val Thr Glu Pro
 35 40 45

10 Asp Ser Phe Thr Thr Phe Leu Asp Leu Val Glu Arg Glu Leu Gly Pro
 50 55 60

15 Leu Asp Ile Leu Val Asn Asn Ala
 65 70

<210> 31

20 <211> 67

<212> PRT

<213> unknown

25 <220>

<221> source

<223> ZF0050310= Arthrobacter paraffineus

30 <400> 31

Ala Thr Asp Gly Ala Arg Val Ala Val Val Asp Leu His Ile Glu Ser
 1 5 10 15

35 Ala Glu Glu Thr Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala
 20 25 30

40 Leu Ala Leu Glu Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala
 35 40 45

45 Phe Glu Ala Thr Val Ala Glu Trp Gly Arg Phe Asp Tyr Leu Val Asn
 50 55 60

50 Asn Ala Gly
 65

<210> 32

55 <211> 67

<212> PRT

<213> unknown

<220>

<221> source

<223> ZF0050310= Arthrobacter paraffineus

5

<400> 32

10

Ala Ala Asp Gly Ala Arg Val Ala Val Val Asp Leu His Ile Glu Ser
 1 5 10 15

Ala Lys Glu Thr Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala
 20 25 30

15

Leu Ala Leu Glu Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala
 35 40 45
 Phe Glu Ala Thr Val Ala Glu Trp Gly Arg Phe Asp Tyr Leu Val Asn
 50 55 60

20

Asn Ala Gly
 65

25

<210> 33

<211> 348

30

<212> PRT

<213> unknown

<220>

35

<221> source

<223> ZF0050310= Arthrobacter paraffineus

<400> 33

40

Met Lys Ala Ile Gln Tyr Ala Arg Ile Gly Ala Glu Pro Glu Leu Thr
 1 5 10 15

45

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
 20 25 30

50

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
 35 40 45

55

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
 50 55 60

Ala Gly Arg Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
 65 70 75 80

	Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Ser	Cys	Trp	
					85					90					95		
5	His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Lys	Glu	Leu	
				100					105					110			
10	Gly	Ile	Asn	Pro	Pro	Gly	Leu	Gly	Ala	Pro	Gly	Ala	Leu	Ala	Glu	Phe	
			115					120					125				
15	Met	Ile	Val	Asp	Ser	Pro	Arg	His	Leu	Val	Pro	Ile	Gly	Asp	Leu	Asp	
		130					135						140				
20	Pro	Val	Lys	Thr	Val	Pro	Leu	Thr	Asp	Ala	Gly	Leu	Thr	Pro	Tyr	His	
	145					150					155					160	
	Ala	Ile	Lys	Arg	Ser	Leu	Pro	Lys	Leu	Arg	Gly	Gly	Ala	Tyr	Ala	Val	
					165					170					175		
25	Val	Ile	Gly	Thr	Gly	Gly	Leu	Gly	His	Val	Ala	Ile	Gln	Leu	Leu	Arg	
				180					185					190			
30	His	Leu	Ser	Ala	Ala	Thr	Val	Ile	Ala	Leu	Asp	Val	Ser	Ala	Asp	Lys	
			195					200					205				
35	Leu	Glu	Leu	Ala	Thr	Lys	Val	Gly	Ala	His	Glu	Val	Val	Leu	Ser	Asp	
		210					215					220					
40	Lys	Asp	Ala	Ala	Glu	Asn	Val	Arg	Arg	Ile	Thr	Gly	Ser	Gln	Gly	Ala	
	225					230					235					240	
	Ala	Leu	Val	Leu	Asp	Phe	Val	Gly	Tyr	Gln	Pro	Thr	Ile	Asp	Thr	Ala	
					245					250					255		
45	Met	Ala	Val	Ala	Gly	Val	Gly	Ser	Asp	Val	Thr	Ile	Val	Gly	Ile	Gly	
				260					265					270			
50	Asp	Gly	Gln	Ala	His	Ala	Lys	Val	Gly	Phe	Phe	Gln	Ser	Pro	Tyr	Glu	
			275					280					285				
55	Ala	Ser	Val	Thr	Val	Pro	Tyr	Trp	Gly	Ala	Arg	Asn	Glu	Leu	Ile	Glu	
		290					295					300					
	Leu	Ile	Asp	Leu	Ala	His	Ala	Gly	Ile	Phe	Asp	Ile	Ala	Val	Glu	Thr	
	305					310					315					320	

	Phe	Ser	Leu	Asp	Asn	Gly	Ala	Glu	Ala	Tyr	Arg	Arg	Leu	Ala	Ala	Gly	
					325					330						335	
5																	
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10																	
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	<211>		348														
15	<212>		PRT														
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20	<221>		source														
	<223>		ZF0050310=		Arthrobacter	paraffineus											
	<400>		34														
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	Glu	Ile	Pro	Lys	Pro	Glu	Pro	Gly	Pro	Gly	Glu	Val	Leu	Leu	Glu	Val	
30				20					25					30			
	Thr	Ala	Ala	Gly	Val	Cys	His	Ser	Asp	Asp	Phe	Ile	Met	Ser	Leu	Pro	
			35					40					45				
35																	
	Glu	Glu	Gln	Tyr	Thr	Tyr	Gly	Leu	Pro	Leu	Thr	Leu	Gly	His	Glu	Gly	
		50					55					60					
40																	
	Ala	Gly	Arg	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile	
	65					70					75					80	
45	Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Ser	Cys	Trp	
					85					90					95		
	His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Lys	Glu	Leu	
50				100					105					110			

	Gly	Ile	Asn	Pro	Pro	Gly	Leu	Gly	Ala	Pro	Gly	Ala	Leu	Ala	Glu	Phe	
			115					120					125				
5	Met	Ile	Val	Asp	Ser	Pro	Arg	His	Leu	Val	Pro	Ile	Gly	Asp	Leu	Asp	
		130					135					140					
10	Pro	Val	Lys	Thr	Val	Pro	Leu	Thr	Asp	Ala	Gly	Leu	Thr	Pro	Tyr	His	
	145					150					155					160	
15	Ala	Ile	Lys	Arg	Ser	Leu	Pro	Lys	Leu	Arg	Gly	Gly	Ala	Tyr	Ala	Val	
					165					170					175		
20	Val	Ile	Gly	Thr	Gly	Gly	Leu	Gly	His	Val	Ala	Ile	Gln	Leu	Leu	Arg	
				180					185					190			
25	His	Leu	Ser	Ala	Ala	Thr	Val	Ile	Ala	Leu	Asp	Val	Ser	Ala	Asp	Lys	
			195					200					205				
30	Leu	Glu	Leu	Ala	Thr	Lys	Val	Gly	Ala	His	Glu	Val	Val	Leu	Ser	Asp	
		210					215					220					
35	Lys	Asp	Ala	Ala	Glu	Asn	Val	Arg	Arg	Ile	Thr	Gly	Ser	Gln	Gly	Ala	
	225					230					235					240	
40	Ala	Leu	Val	Leu	Asp	Phe	Val	Gly	Tyr	Gln	Pro	Thr	Ile	Asp	Thr	Ala	
					245					250					255		
45	Met	Ala	Val	Ala	Gly	Val	Gly	Ser	Asp	Val	Thr	Ile	Val	Gly	Ile	Gly	
				260					265					270			
50	Asp	Gly	Gln	Ala	His	Ala	Lys	Val	Gly	Phe	Phe	Gln	Ser	Pro	Tyr	Glu	
			275					280					285				
55	Ala	Ser	Val	Thr	Val	Pro	Tyr	Trp	Gly	Ala	Arg	Asn	Glu	Leu	Ile	Glu	
		290					295					300					
60	Leu	Ile	Asp	Leu	Ala	His	Ala	Gly	Ile	Phe	Asp	Ile	Ala	Val	Glu	Thr	
	305					310					315					320	
65	Phe	Ser	Leu	Asp	Asn	Gly	Ala	Glu	Ala	Tyr	Arg	Arg	Leu	Ala	Ala	Gly	
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70	Thr	Leu	Ser	Gly	Arg	Ala	Val	Val	Val	Pro	Gly	Leu					
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 5 <212> DNA
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 10 <220>
 <221> source
 <223> ZF0002326= Actinoplanes missouriensis; ZF0003505= Streptomyces;
 15 ZF0050197= Pseudomonas oleovorans; ZF0050294= Rhodococcus;
 ZF0050330= Bacillus; ZF0051303= Bacterium; ZF0051337=
 Methylobacter; ZF0051321= Bacterium; ZF0050782= Lactobacillus
 bulgaricus; ZF0050544= Phyllobacterium rubiacearum; ZF0002852=
 Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862=
 20 Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0002031=
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
 Streptomyces; ZF0002437= Streptomyces; ZF0003712=
 Micromonospora; ZF0003765= Streptomyces; ZF0051305= Bacterium;
 ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018=
 Streptomyces; ZF0003767= Actinomyces; ZF0002332= Streptomyces
 25 diastatochromogenes; ZF0003768= Actinomyces; ZF0002379=
 Streptomyces coelestis; ZF0002351= Nonomuraea roseoviolacea;
 ZF0003769= Actinomyces;
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 35 ttcatgatcg tcgattctcc tcgccacctt gtcccgatcg gtgacctega cccggtcaag
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 40 240
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 300
 45 attcagctcc tccgtcacct ctccggcgtca acggtcatcg ctttggacgt gagcgccgac
 360
 aagctcgaac tggcaaccaa ggtaggcgct cacgaagtgg ttctgtccga caaggacgcg
 420
 50 gccgagaacg tccgcaagat cactggaagt caaggcgccg cactggttct cgacttcgtt
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 55 488
 <210> 36

<211> 385
 <212> DNA
 5 <213> unknown
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 10 <223> ZF0002326= Actinoplanes missouriensis; ZF0003505= Streptomyces;
 ZF0050197= Pseudomonas oleovorans; ZF0050294= Rhodococcus;
 ZF0050330= Bacillus; ZF0051303= Bacterium; ZF0051337=
 15 Methylomonas; ZF0051321= Bacterium; ZF0050782= Lactobacillus
 bulgaricus; ZF0050544= Phyllobacterium rubiacearum; ZF0002852=
 Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862=
 Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0002031=
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
 Streptomyces; ZF0002437= Streptomyces; ZF0003712=
 20 Micromonospora; ZF0003765= Streptomyces; ZF0051305= Bacterium;
 ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018=
 Streptomyces; ZF0003767= Actinomyces; ZF0002332= Streptomyces
 diastatochromogenes; ZF0003768= Actinomyces; ZF0002379=
 Streptomyces coelestis; ZF0002351= Nonomuraea roseoviolacea;
 ZF0003769= Actinomyces;
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 30 120
 ttcatgatcg tcgattctcc tcgccacctt gtcccgatcg gtgacctcga cccgggtcaag
 180
 35 acggtgcccgc tgaccgacgc cgggtctgacg ccgtatcacg cgatcaagcg ttctctgccg
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 aaacttcgcg gaggtctgta cgcggttggtc attggtaccg gcggggtcgg ccacgtcacc
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 40 attcagctcc tccgtcacct ctcgggcgga acggtcatcg ctttggacgt gagcgcgga
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 45 385
 <210> 37
 50 <211> 486
 <212> DNA
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 55 <220>
 <221> source
 <223> ZF0050286= Corynebacterium hoagii

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 5 cgcgcaaggg aactcggcat cgccccaccc ggcttgggcg cgccggggcg gatcgccgag
 120
 10 tacatgatcg tcgactcgcc gcgtcacctg gtcccgatcg gtgacctga ccccgtcacg
 180
 acggtgccgc tgaccgacgc cgggctcacc ccgtaccacg cgatcaaacg gtcgctcggc
 240
 15 aagctccgcg ccggctcgta cgcagtcgtg atcggcaccg gaggcctcgg acacgtcggc
 300
 atccagctgc tccgccacct gtcccctgca cgcacatcg ccctcgacgt caacgacgag
 360
 20 aagctcgcg tgcgccgga ggctggcgcg cacgagaccg tgttgtcgaa cgccgacgcc
 420
 25 gccgcgaacg tccggaagat cacgggttcg gccggtgccg cgctggctct agacttcgtc
 480
 ggctac
 486
 30
 <210> 38
 <211> 483
 35 <212> DNA
 <213> unknown
 <220>
 40
 <221> source
 <223> ZF0050310= *Arthrobacter paraffineus*
 <400> 38
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 cgggcaaaaag aactcggcat caatcctcct ggtctcgggtg caccgggcgc gttggccgaa
 120
 50 ttcatgatcg tcgattcacc tcgccacctc gtcccgatcg gcgacctga tccggtcaag
 180
 acggtgccac tgaccgacgc cgggtctgact ccgtatcacg cgatcaagcg ttcactgccg
 240
 55 aaacttcgcg gtggcgcgta cgccgtcgtc atcgggtaccg gcgggtctcgg ccatgtcgcc
 300

atccaactcc tccgccacct ctcggcagca accgtcatcg cactcgacgt gagcgcgga
360

5 aagctcgtagc tggcaaccaa ggtaggcggt cacgaagtgg tcctgtccga caaggacgag
420

gcccagaacg tccgcaggat caccggaagt cagggcgccg cactggttct tgacttcgtt
480

10 ggc
483

15 <210> 39
<211> 210
<212> DNA

20 <213> unknown
<220>
<221> source

25 <223> ZF0004210= Actinomyces; ZF0004212= Actinomyces; ZF0004211=
Actinomyces; ZF0003860= Actinomyces; ZF0004218= Actinomyces;
ZF0003868= Actinomadura; ZF0004213= Actinomyces; ZF0003876=
Actinomyces; ZF0003866= Actinomyces; ZF0003864= Actinomyces;
ZF0003862= Actinomadura; ZF0003869= Actinomyces; ZF0003867=
30 Actinomadura; ZF0004216= Actinomyces; ZF0004235= Actinomyces;
ZF0004209= Actinomadura; ZF0004214= Actinomyces; ZF0003871=
Actinomyces; ZF0004063= Actinomadura; ZF0004052= Actinomadura;
ZF0006405= Streptomyces; ZF0003865= Actinomadura; ZF0004047=
Actinomadura; ZF0004070= Actinomyces; ZF0004085= Actinomyces;
35 ZF0004217= Actinomyces; ZF0004089= Actinomadura; ZF0004090=
Actinomadura; ZF0006138= Streptomyces; ZF0004236= Actinomadura;
ZF0051203= Bacterium;

40 <400> 39
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60

cgcgccaagg aactcgcat cgccccgcc ggactcggct cgcccgccgc catggccgag
120

45 tacatgatcg tcgacgaccc gcgccacctg gtgccgctcg gcggtctcga cccggtccag
180

50 gccgtgccgc tcaactgacgc gggcctgaca
210

55 <210> 40
<211> 282
<212> DNA
<213> unknown

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<220>

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5 <223> ZF0002326= Actinoplanes missouriensis; ZF0003505= Streptomyces;
      ZF0051321= Bacterium; ZF0050782= Lactobacillus bulgaricus;
      ZF0050544= Phyllobacterium rubiacearum; ZF0002031=
      Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
10 Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;
      ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=
      Actinoplanes philippinensis; ZF0002441= Streptomyces;
      ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=
      Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=
15 Micromonospora; ZF0004980= Streptomyces; ZF0004821=
      Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396=
      Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces;
      ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087=
      Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium;
20 ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538=
      Actinomyces; ZF0003535= Actinomyces;

<400> 40
      tgtcacaccg atcaccacat cgtcaccggc gcgaccccgga tgccgctcgtt cccgggtcatg
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25      ggcgggcacg aggggttcggg cgtcatcacc aagctcggcc ctgaggtcaa gggactggag
      120
      gtcggcgacc acgtcgttct gtccttcatt ccggcttggtg gaacctgtcc ggcgtgttcg
30      180
      gccgggcatc agaatctttg tgacctcggg atgggcctcc tcagcggcca agccatcagc
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35      gacggcacgt accggatcca ggctcgcggc gaaaacgtga tc
      282

<210> 41
40 <211> 276
      <212> DNA
45 <213> unknown

<220>

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      ZF0050544= Phyllobacterium rubiacearum; ZF0002031=
      Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
      Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;
55 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=
      Actinoplanes philippinensis; ZF0002441= Streptomyces;
      ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=
      Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=
      Micromonospora; ZF0004980= Streptomyces; ZF0004821=

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Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396= Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces; ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087= Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium; ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538= Actinomyces; ZF0003535= Actinomyces;

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 120

ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180

ggacagagca acctctgca cctcgggccc attctgatgg ccggcgacaca ggtcgacggg
 240

acgtaccgcg cgacagctcg cgggcacgac gtcgga
 276

<210> 42

<211> 276

<212> DNA

<213> unknown

<220>

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 120

ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180

ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg
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5 acgtaccgcg cgacagctcg cgggcacgac gtcgga
 276

10 <210> 43
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15 <213> unknown
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 ZF0051321= Bacterium; ZF0050782= Lactobacillus bulgaricus;
 ZF0050544= Phyllobacterium rubiacearum; ZF0002031=
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
 Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;
 25 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=
 Actinoplanes philippinensis; ZF0002441= Streptomyces;
 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=
 Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=
 Micromonospora; ZF0004980= Streptomyces; ZF0004821=
 30 Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396=
 Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces;
 ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087=
 Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium;
 ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538=
 35 Actinomyces; ZF0003535= Actinomyces;

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 120

45 ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180

ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg
 240

50 acgtaccgcg cgacagctcg cgggcacgac gtcgga
 276

55 <210> 44
 <211> 276
 <212> DNA

<213> unknown

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 ZF0050544= Phyllobacterium rubiacearum; ZF0002031=

10 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
 Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;
 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=
 Actinoplanes philippinensis; ZF0002441= Streptomyces;

15 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=
 Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=
 Micromonospora; ZF0004980= Streptomyces; ZF0004821=
 Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396=
 Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces;
 ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087=
 Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium;
 ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538=
 20 Actinomyces; ZF0003535= Actinomyces;

<400> 44
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 120

30 ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180

ggacagagca acctctgcga cctcgggcgc attctgatgg cgggcgcacg ggtcgacggg
 240

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 276

<210> 45

40 <211> 276

<212> DNA

45 <213> unknown

<220>

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 ZF0050544= Phyllobacterium rubiacearum; ZF0002031=

55 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
 Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;
 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=
 Actinoplanes philippinensis; ZF0002441= Streptomyces;
 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=
 Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=
 Micromonospora; ZF0004980= Streptomyces; ZF0004821=

Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396=
 Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces;
 ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087=
 Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium;
 5 ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538=
 Actinomyces; ZF0003535= Actinomyces;

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 120
 15 ggcatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180
 ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtagacggg
 240
 20 acgtaccgcg cgacagctcg cgggcacgac gtcgga
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 25 <211> 279
 <212> DNA
 <213> unknown
 30 <220>
 <221> source
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 40 ggccacgaag gagcgggggt ggtagaggcc gtcggctcgt cgatcgacag cattgcgccc
 120
 ggtgatcacg tgttgctgag ctaccgcagt tgcggtgtgt gcaggcagtg cctcagcggg
 180
 45 catcgggctg actgcgaaag ctcacacggg ctcaacagct ctggcgacag caccgacggc
 240
 tcgacgccg tccggcgaag cggaactccg atacgggtcc
 50 279
 <210> 47
 55 <211> 279
 <212> DNA
 <213> unknown

<220>

<221> source

5 <223> ZF0002333= Rhodococcus erythropolis

<400> 47

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10 ggacacgaag ggcgcggcgt cgtgcaagcc gttggctcgt cgatcgacaa catcgcgggt
120

ggatgatcacg tattgctgag ctaccgcagt tgcgggtgtat gcaggcaatg tctcagcgac
15 180

catcggggcgt actgcgaaa ctcacacggg ctcaacagct ctggcgacag caccgacggc
240

20 tgcacgcccgg tccggcgaaa cggaactccg atacggtcc
279

<210> 48

25 <211> 360

<212> DNA

<213> unknown

30 <220>

<221> source

<223> ZF0051303= Bacterium; ZF0051337= Methylobacter; ZF0002862= Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0051305= Bacterium; ZF0003513= Actinomyces; ZF0002351= Nonomuraea roseoviolacea; ZF0003769= Actinomyces; ZF0002017= Streptomyces; ZF0051306= Bacterium; ZF0002016= Streptomyces; ZF0003504= Actinomyces; ZF0006073= Streptomyces; ZF0003770= Actinomyces; ZF0002352= Actinoplanes italicus; ZF0002378= Streptomyces aureomonopodiales; ZF0006089= Streptomyces; ZF0006106= Streptomyces; ZF0051325= Bacterium; ZF0006108= Streptomyces; ZF0002440= Streptomyces; ZF0051302= Bacterium; ZF0003532= Actinomyces; ZF0003548= Nocardiaform;

35

40

45 <400> 48

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50 cacctcgtcc tcgggcacga atcgttgggc cgagtacgca ccgcgcccga cggcagcgggt
120

ttcgccgccg gtgatctcgt cgtcgggatc gtgcgcaggc ccgatccggt gccgtgcggg
180

55 gcgtgtgcgc acggtgagtt cgacatgtgc cgcaacgggt agtacgtcga gcgcggggatc
240

aagcagatcg acgggtacgg gtcgacgtcg tgggtggtgg acgccgacta cacggtcaag
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 ctggacccgg cgctcacga ggtgggtgtg ctgatggaac cgacgacggt gcttggccaa
 5 360
 <210> 49
 10 <211> 421
 <212> DNA
 <213> unknown
 15 <220>
 <221> source
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 20 Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0051305=
 Bacterium; ZF0003513= Actinomyces; ZF0002351= Nonomuraea
 roseoviolacea; ZF0003769= Actinomyces; ZF0002017= Streptomyces;
 ZF0051306= Bacterium; ZF0002016= Streptomyces; ZF0003504=
 Actinomyces; ZF0006073= Streptomyces; ZF0003770= Actinomyces;
 25 ZF0002352= Actinoplanes italicus; ZF0002378= Streptomyces
 aureomonopodiales; ZF0006089= Streptomyces; ZF0006106=
 Streptomyces; ZF0051325= Bacterium; ZF0006108= Streptomyces;
 ZF0002440= Streptomyces; ZF0051302= Bacterium; ZF0003532=
 Actinomyces; ZF0003548= Nocardiaform;
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 35 ccgctcacgc tcggccacga gtctcgctggc gaggtcgctg agaccggccg cgacgtgacc
 120
 gacatccagg tcggcgacct ggtcagcggc gagggccacc tggctctgctg caagtgccg
 180
 40 aactgcctgg ccggccgccc tcacctgtgc cgcgcgaccg tcggcctcgg tgcggccgct
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 gacggcgcct tcgccgagta cgtggtgctg cccgcctcca acgtgtgggt gcaccgggtg
 45 300
 ccggtcgacc tcgacgtcgc cgcgatcttc gaccggttcg gcaacgcggt gcacaccg
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 421
 55
 <210> 50
 <211> 414

<212> DNA
 <213> unknown
 5 <220>
 <221> source
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 ZF0050330= Bacillus, ZF0002852= Rhodococcus; ZF0050310=
 Arthrobacter paraffineus; ZF0002437= Streptomyces; ZF0003712=
 Micromonospora; ZF0003765= Streptomyces; ZF0002332=
 Streptomyces diatsatochromogenes; ZF0003768= Actinomyces;
 15 ZF0002379= Streptomyces coelestis; ZF0002443= Streptomyces;
 ZF0002442= Streptomyces; ZF0002436= Streptomyces; ZF0050994=
 Bacterium; ZF0050992= Bacterium; ZF0050442= Bacterium;
 ZF0002049= Streptomyces; ZF0006069= Streptomyces; ZF0006075=
 Streptomyces; ZF0004724= Nocardiaform; ZF0002392= Actinoplanes
 nipponensis; ZF0002356= Actinoplanes brasiliensis; ZF0003501=
 20 Actinomyces; ZF0051322= Bacterium; ZF0006078= Streptomyces;
 ZF0006092= Streptomyces; ZF0006090= Streptomyces; ZF0006084=
 Streptomyces; ZF0006068= Streptomyces; ZF0050284= Rhodococcus;
 ZF0050028= Agrobacterium tumefaciens; ZF0003540= Actinomyces;
 25 ZF0003528= Actinomyces; ZF0003529= Actinomyces;
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 180
 35 ggctgccatg gataccgggc caccggccgc tggcgctttg gcaacatcat cgatggcgcc
 240
 caggccgaat acctgctggt tcccgatgag cagggaatc tggcgccggt tccggacaac
 40 300
 ctgagcgatg aacaggtgct gatgtgccc gacatcatgt ccaccggctt caaaggcgca
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 <210> 51
 50 <211> 432
 <212> DNA
 55 <213> unknown
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 ZF0050330= Bacillus, ZF0002852= Rhodococcus; ZF0050310=
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 Micromonospora; ZF0003765= Streptomyces; ZF0002332=
 5 Streptomyces diatsatochromogenes; ZF0003768= Actinomyces;
 ZF0002379= Streptomyces coelestis; ZF0002443= Streptomyces;
 ZF0002442= Streptomyces; ZF0002436= Streptomyces; ZF0050994=
 Bacterium; ZF0050992= Bacterium; ZF0050442= Bacterium;
 ZF0002049= Streptomyces; ZF0006069= Streptomyces; ZF0006075=
 10 Streptomyces; ZF0004724= Nocardiaform; ZF0002392= Actinoplanes
 nipponensis; ZF0002356= Actinoplanes brasiliensis; ZF0003501=
 Actinomyces; ZF0051322= Bacterium; ZF0006078= Streptomyces;
 ZF0006092= Streptomyces; ZF0006090= Streptomyces; ZF0006084=
 Streptomyces; ZF0006068= Streptomyces; ZF0050284= Rhodococcus;
 15 ZF0050028= Agrobacterium tumefaciens; ZF0003540= Actinomyces;
 ZF0003528= Actinomyces; ZF0003529= Actinomyces;

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 25 180
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 300
 gacggtgtga gcgacgagca gatgctcatg ctgcgccaca tcctgcccac ctccctacgag
 35 360
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 55 <223> ZF0050310= Arthrobacter paraffineus

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tcacgagcgc gtcacgtccg agattcagct caacatcgcc acgctggtcg agctgacaca
120

5 cacattcccg cccgaccttc tcaccggccg cggagcactg gtcaacatcg ccagcacagc
180

gtcgttccag ccgacaccgg gcatggccgt ctactgcgct
220

10

<210> 53

<211> 226

15 <212> DNA

<213> unknown

20 <220>

<221> source

<223> ZF0050310= *Arthrobacter paraffineus*

25 <400> 53

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60

tctcgagcgc gtcacgtccg agattcagct caacatcgcc acgctggtcg agctgacaca
30 120

cacattcctg cccgaccttc tcaccggccg cggagcactg gtcaacatcg ccagcacagc
180

35 gtcgttccag ccgacaccgg gcatggccgt ctactgcgcc accaag
226

<210> 54

40 <211> 237

<212> DNA

45 <213> unknown

<220>

<221> source

50 <223> ZF0003535= *Actinomyces*

<400> 54

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55 acccccgccg attttgagcg catcctgcgg gtgaacctga ccggcgtctt caacctgagc
120

caagccgtca ttcccttgat gattcagcgc ggccggaggaa gcatcgtctc gatttctctg
 180
 ctgtcggcgc agaacggcgg ggggatcttc ggccggcgccc actattgcgc aaccaag
 5 237
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 10 <211> 229
 <212> DNA
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 15 <220>
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 20 <400> 55
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 25 gccgctaaag gactggcaga ccatgggtgaa caccaacatc accggtctac tgaacatcac
 120
 ccaccatctc ctgccgacac tgategaccg taaaggtatc gtcgtcaacc tttcgtctgt
 180
 30 tgccgcgcac tatccctata cgggcggcaa tgtatactgc gcctccaag
 229
 35 <210> 56
 <211> 216
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 40 <213> unknown
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 45 <221> source
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 50 60
 ggcgacatcg acgaagccac tctcgcgcga gcagccaagg atttgggcat ccgcacgttc
 120
 55 gggcgctctg acgtcaccga cccgcctctg ttcttcgact tcctcgacac cgtcgaaggt
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 gaactcggcc cgatcgacgt gctgatcaac aacgcg
 216

<210> 57

5 <211> 225

<212> DNA

<213> unknown

10 <220>

<221> source

<223> ZF0080310= *Arthrobacter paraffineus*

15 <400> 57

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60

20 ggcgacatca acgaaaccgt gggaacggct gcggtcgccg aactcgggtg agagtcgggtc
120

gcccgtttcg cttcctgcga cgtgcgtgac tccggacagg tcgaggccat gctcgatctg
180

25 gccgaaagcg ctttcgggtcc agtcgatgtc atgatgaaca acgcg
225

<210> 58

30 <211> 216

<212> DNA

<213> unknown

<220>

<221> source

40 <223> ZF0080310= *Arthrobacter paraffineus*

<400> 58

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60

45 ggcgacatcg acgaggcacg tgctaaggag accgccgccg aactgggggt taaggttgtc
120

50 acccgctcgt atgtcaccga ccttgactcg ttcaaagact ttctcgacct agtcgaggga
180

gacctcggcc cctcgcacgt gctgatcaac aacgcg
216

55 <210> 59

<211> 222

<212> DNA

<213> unknown

5 <220>

<221> source

<223> ZF0080310= *Arthrobacter paraffineus*

10 <400> 59
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gacatcaacg aaaccgtggg aacggctgcg gtcgccgaac tcggtggaga gtcggtcgcc
15 120
cgtttcgctt cctgcgacgt gcgtgactcc ggacaggtcg aggccatgct cgatctggcc
180
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20 222
<210> 60
<211> 222

25 <212> DNA
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30 <220>

<221> source

<223> ZF0080310= *Arthrobacter paraffineus*

35 <400> 60
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60
atcaacgaaa ccgtgggaac ggctgcggtc ggcgaaactcg gtggagagtc ggtcgcccgt
40 120
ttcgcttctt gcgacgtgcg tgactccgga caggtcgagg ccatgctcga tctggccgaa
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agcgcctttcg gtccagtcga tgtcatggtc aacaacgccg gc
45 222
<210> 61

50 <211> 186
<212> DNA

55 <213> unknown
<220>
<221> source

<223> ZF0002333= Rhodococcus erythropolis

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gaatcgcagt acggcacacc cgcgctcgcc cttgaggccg atgtgcgcga ccgcgccgcc
120

10 gtgagcgccg ctttcgaagc caccgtcgcc gaatggggac gcttcgacta cctcgtcaac
180

aacgcc
186

15

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<211> 222

20 <212> DNA
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<220>

25 <221> source
<223> ZF0002333= Rhodococcus erythropolis .

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ctcgatcccg aacctgccgc tcagaccgag cgcgatatca aagccacagg tggacaggct
120

35 gtctcgtgcg tcggctccgt tgccgaggac gggttcgccg aacgcttcgt gaacactgcc
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gtcgaatcat tcggcggact cgacgtcatg gtgaacaacg cg
40 222

<210> 63

45 <211> 231

<212> DNA

<213> unknown

50 <220>

<221> source
<223> ZF0002333= Rhodococcus erythropolis

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60

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gtcgccaggc gggcagatcg cctcgaagcc ctcgctaccg aactccgcgt cgcccacggc
120

atcacagtca cagttctgcc tgccgacctg gcggcgcccg gcgtcggcgc aacactgcac
5 180

caggagctga caagccgtgg catcacctgc acctcgctga tcaacaacgc c
231

10 <210> 64
    <211> 216

15 <212> DNA
    <213> unknown
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20 <221> source
    <223> ZF0003535= Actinomyces

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    60

gtcgacatcg acgaggcacg tgcgaagggg gccgccgccg aactcggggg gaaggtcgtc
120
30 acccgactcg acgtcaccga acctgactcg ttcacaacgt ttctggacct ggtcgaacgt
    180

gaactcggac ccctcgacat cctgggtcaac aacgcg
35 216

    <210> 65

40 <211> 201
    <212> DNA
    <213> unknown
45 <220>

    <221> source
    <223> ZF0050310= Arthrobacter paraffineus
50 <400> 65
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    60

55 gtcgcactta tcgaatcgca gtacggcaca cccgcgctcg cccttgaggc cgatgtgcgc
    120

gaccgcgccg ccgtgagcgc cgctttcgaa gccaccgtcg ccgaatgggg acgcttcgac
180

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tacctcgtca acaacgccgg c
201

5
<210> 66
<211> 201

10
<212> DNA
<213> unknown
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15
<221> source
<223> ZF0050310= *Arthrobacter paraffineus*

20
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gtcgcactta tcgaatcgca gtacggcaca cccgcgctcg cccttgaggc cgatgtgcgc
120

25
gaccgcgccg ccgtgagcgc cgctttcgaa gccaccgtcg ccgaatgggg acgcttcgac
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30
tacctcgtca acaacgccgg c
201

35
<210> 67
<211> 1047
<212> DNA
<213> unknown

40
<220>

45
<221> source
<223> ZF0050310= *Arthrobacter paraffineus*

50
<400> 67
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cccgcgcccg gtccaggtga agtgctcctg gaagtcaccg ctgccggcgt ctgccactcg
120
gacgacttca tcatgagcct gcccgagag cagtacacct acggccttcc tctcacgctc
180

55
ggccacgaag gcgcggccg ggtcgccgcc gtcggcgagg gcgtcgaagg actcgacatc
240
ggaaccaatg tcgtcgtcta cggaccctgg ggctgtggca gctgttggca ctgctcgcaa
300

ggactcgaaa actactgttc tcgggcaaaa gaactcggca tcaatcctcc tggctcgggt
 360
 5 gcacccggcg cggtggccga attcatgata gtcgattcac ctgccacct cgtcccgatc
 420
 ggcgacctcg atccgggtcaa gacgggtgcca ctgaccgacg ccgggtctgac tccgtatcac
 480
 10 gcgatcaagc gttcactgcc gaaacttcgc ggtggcgcggt acgccgtcgt catcggtacc
 540
 ggcggtctcg gccatgtcgc catccaactc ctccgccacc tctcggcagc aaccgtcatc
 600
 15 gcactcgacg tgagcgcgga caagctcgaa ctggcaacca aggtaggcgc tcacgaagtg
 660
 20 gtcctgtccg acaaggacgc ggccgagaac gtccgcagga tcaccggaag tcagggcgcc
 720
 gcactgggtc tcgacttcgt cggctatcag cccaccatcg acaccgcgat ggctgtcgcc
 780
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 840
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 900
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 960
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 cccgagcccc gtccaggatga agtgctcctg gaagtcaccg ctgccggcgt ctgccactcg
 120

gacgacttca tcatgagcct gcccgaagag cagtacacct acggccttcc tctcacgctc
 180
 5 ggccacgaag gcgccggccg ggtcgccgcc gtcggcgagg gcgtcgaagg actcgacatc
 240
 ggaaccaatg tcgtcgtcta cggaccctgg ggctgtggca gctgttggca ctgctcgcaa
 300
 10 ggactcgaaa actactgttc tcgggcaaaa gaactcggca tcaatcctcc tggctcgggt
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 gcacccggcg cgttggccga attcatgata gtcgattcac ctcgccacct cgtcccgatc
 420
 15 ggcgacctcg atccgggtcaa gacggtgcc a ctgaccgacg ccggtctgac tccgtatcac
 480
 gcgatcaagc gttcactgcc gaaacttcgc ggtggcgcggt acgccgtcgt catcggtacc
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 20 ggcggtctcg gccatgtcgc catccaactc ctccgccacc tctcggcagc aaccgtcatc
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 gcactcgacg tgagcgcgga caagctcgaa ctggcaacca aggtaggcgc tcacgaagtg
 660
 25 gtctgtccg acaaggacgc ggccgagaac gtccgcagga tcaccggaag tcagggcgcc
 720
 gcactgggttc tcgacttcgt cggctatcag cccaccatcg acaccgcgat ggctgtcgcc
 780
 ggcgctcgat cggacgtcac gatcgtcggg atcggcgacg ggcaggccca tgccaaagtc
 840
 35 gggttcttcc aaagtcctta cgaggcttct gtgacagttc cgtactgggg tgcccgaac
 900
 gagctgatcg aattgatcga cctggcgcac gccggcatct tcgacatcgc ggtggagacc
 960
 40 ttcagtctcg acaacggcgc cgaagcgtat cgacgactgg ccgccggaac gctcagcggc
 1020
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